#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/095,385

DATE: 06/17/98 TIME: 10:43:30

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This Raw Listing contains the General Information Section and up to the first 5 pages.

#2

#### 1 SEQUENCE LISTING 2 3 General Information (1) ENTERED 4 5 (i) APPLICANT: Morrison, Sherie L. Chintalacharuvu, Kote R. 6 7 (ii) TITLE OF THE INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED 8 9 BY SINGLE CELLS AND METHODS FOR MAKING AND USING 10 SAME 11 12 (iii) NUMBER OF SEQUENCES: 4 13 (iv) CORRESPONDENCE ADDRESS: 14 (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt 15 (B) STREET: 11150 Santa Monica Boulevard, Suite 400 16 17 (C) CITY: Los Angeles 18 (D) STATE: CA (E) COUNTRY: USA 19 (F) ZIP: 90025 20 21 22 (V) COMPUTER READABLE FORM: 23 (A) MEDIUM TYPE: Diskette 24 (B) COMPUTER: IBM Compatible 25 (C) OPERATING SYSTEM: DOS 26 (D) SOFTWARE: FastSEQ for Windows Version 2.0 27 (vi) CURRENT APPLICATION DATA: 28 (A) APPLICATION NUMBER: 29 (B) FILING DATE: 09-JUN-1998 30 31 (C) CLASSIFICATION: 32 33 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 60/050,969 34 35 (B) FILING DATE: 19-JUN-1997 36 37 38 39 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Canady, Karen S 40 41 (B) REGISTRATION NUMBER: 39,927 42 (C) REFERENCE/DOCKET NUMBER: 30435.45USU1 43 (ix) TELECOMMUNICATION INFORMATION: 44 (A) TELEPHONE: 310 445-1140 45 (B) TELEFAX: 310 445-9031 46

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47	(C) TELEX:	
48		
49		
50	(2) INFORMATION FOR SEQ ID NO:1:	
51		
52	(i) SEQUENCE CHARACTERISTICS:	
53	(A) LENGTH: 30 base pairs	
54	(B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: double	
56	(D) TOPOLOGY: linear	
57		
58	(ii) MOLECULE TYPE: cDNA to mRNA	
59		
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
61		
62	GGGCAGAACG GTGACCATCA ACTGCCCTTT	30
63		
64	(2) INFORMATION FOR SEQ ID NO:2:	
65		
66	(i) SEQUENCE CHARACTERISTICS:	
67	(A) LENGTH: 42 base pairs	
68	(B) TYPE: nucleic acid	
69	(C) STRANDEDNESS: double	
70	(D) TOPOLOGY: linear	
71		
72	(ii) MOLECULE TYPE: cDNA to mRNA	
73		
74	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
75		
76	AAGGAATTCC TACTCTGCAA AAAGCCTGGG GTCCTGAATG GC	42
77		
78	(2) INFORMATION FOR SEQ ID NO:3:	
79		
80	(i) SEQUENCE CHARACTERISTICS:	
81	(A) LENGTH: 1839 base pairs	
82	(B) TYPE: nucleic acid	
83	(C) STRANDEDNESS: double	
84	(D) TOPOLOGY: linear	
85		
86	(ii) MOLECULE TYPE: cDNA to mRNA	
87		
88	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
89		
90	ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACGAAGAGT	60
91	CCCATATTTG GTCCCGAGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTC CATCACGTGC	120
92	TACTACCCAC CCACCTCTGT CAACCGGCAC ACCCGGAAGT ACTGGTGCCG GCAGGGAGCT	180
93	AGAGGTGGCT GCATAACCCT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGCAGGC	240
94	AGGGCTAACC TCACCAACTT CCCGGAGAAC GGCACATTTG TGGTGAACAT TGCCCAGCTG	300
95	AGCCAGGATG ACTCCGGGCG CTACAAGTGT GGCCTGGGCA TCAATAGCCG AGGCCTGTCC	360
96	TTTGATGTCA GCCTGGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC	420
97	ACAGTGGACC TGGGCAGAAC GGTGACCATC AACTGCCCTT TCAAGACTGA GAATGCTCAA	480
98	AAGAGGAAGT CCTTGTACAA GCAGATAGGC CTGTACCCTG TGCTGGTCAT CGACTCCAGT	540
99	GGTTATGTGA ATCCCAACTA TACAGGAAGA ATACGCCTTG ATATTCAGGG TACTGGCCAG	600

150 151

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										ET: S267	
100	TTACTGTTCA										660
101	CAGGCTGGGG										720
102	GAGCCCGAGC										780
103	CCTGAGGTGG										840
104	GTGGTCGTCA										900
105	CCCCAGGACA										960
106	GGGCGCTACC										1020
107	GCCTGGCAAC										1080
108 .	GGGGTGGCAG										1140
109	ATCAAGTACT										1200
110	AGCGAGGGGT										1260
111	AACGGCACCT										1320
112	TGTCTGACCA										1380
113	GAACCAAACC										1440
114	CCCTGTCACT										1500
115	ACGGGCTGCC	AGGCCCTGC	C CAGCCA	AGAC	GAAGGC	CCA	GCAAGGCC	TT	CGTG	ACTGT	1560
116	GACGAGAACA										1620
117	TGGTACTGGT										1680
118	GCAGTTGAAG										1740
119	GCTCCTGATG						TTGAGAAC	'AA	AGCC!	ATTCAG	1800
120	GATCCCAGGC	TTTTTGCAG	A GTAGGA	ATTC	CTGCAG	CC					1839
121											
122	(:	2) INFORMA	TION FOR	SEQ	ID NO:	<b>:</b>					
123											
124	` '	SEQUENCE C									
125	•	) LENGTH:			ids						
126	•	TYPE: am									
127	•	) STRANDED			1						
128	( D	) TOPOLOGY	: linear					•			
129											
130	(11)	MOLECULE '	TYPE: pr	oteir	1					•	
131		GEOMENIAE :			GEO T.	WO . 4					
132	(X1)	SEQUENCE	DESCRIPT	TON:	SEQ ID	NO:4	•				
133	Met Leu Lei	. Dhe well	ra. Mb.	G T	T	31- 1	val Dha	D	31-	710	
134		i Phe vai i	Leu Thr	cys I		ATA V	vai Phe	Pro	15	тте	
135 136	l Ser Thr Lys	_	Tlo Dho	01 · · · ·	10	al., s	val Aan	202		alu.	
136	ser in Ly.	20 PIO .	ire Phe	_	25	GIU V	val ASII	30	vaı	GIU	
137	Gly Asn Ser		rlo mbr	_		Dro I	Oro Mbr		1701	λan	
139	_	val Ser	rre int		ryr Tyr			Ser	vaı	ASII	
140	Arg His Th		Trr Tr					C1 11	. cl.,	Cvc	
141	50	Arg Lys	191 11D 55	Cys A	arg Grii	_	Ala Alg 60	СТУ	GLY	Cys	
141	Ile Thr Let	, Tlo Cor		C1 11 T	Tur Val			Tir	λla	Gl v	
142	65		70	GIY I	yr var	75	ser Lys	ıyı	АТа	80 80	
143	Arg Ala Ası		. •	Dro C	מאל ווני		Thr Dha	Va1	V=1		
144	ALY ALA ASI	n Leu Thi A	non FNE	PIO G	90	оту	IIII FIIE	val	95	Hall	
145	Ile Ala Gli		aln Aen	Nen e		Ara 9	Tur Tue	Cue		Τ. Δ11	
147	TTE WTG OT	100	ern wab	_	lO5	ALY .	туг гуз	110	_	nea.	
148	Gly Ile Ası		יום.ז ערם		-	val 🤇	Ser Len			Ser	
149	115	-	Gry neu	120	TIE MOD	AGT -	125	310	· val	Der	
* T J	11:	,		120			123				

Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu 130 135 140

Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln

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														TIVE	UIS	L. 1. 32
153	145					150					155					160
154	Lys	Arg	Lys	Ser	Leu	Tyr	Lys	Gln	Ile	Gly	Leu	Tyr	Pro	Val	Leu	Val
155					165					170					175	
156	Ile	Asp	Ser	Ser	Gly	Tyr	Val	Asn	Pro	Asn	Tyr	Thr	Gly	Arg	Ile	Arg
157				180					185					190		
158	Leu	Asp	Ile	Gln	Gly	Thr	Gly	Gln	Leu	Leu	Phe	Ser	Val	Val	Ile	Asn
159		-	195		-		-	200					205			
160	Gln	Leu	Ara	Leu	Ser	Asp	Ala	Glv	Gln	Tvr	Leu	Cys	Gln	Ala	Glv	Asp
161		210	5			_	215			-		220				•
162	Asp	-	Asn	Ser	Asn	Lvs		Asn	Ala	Asp	Leu	Gln	Val	Leu	Lvs	Pro
163	225					230	-1-				235				-1-	240
164		Pro	Glu	Leu	Val	-	Glu	Asp	Leu	Ara		Ser	Val	Thr	Phe	-
165					245	- 1 -		E		250	1				255	
166	Cvs	Δla	T.e.11	Glv		Glu	Val	Δla	Δsn		Δla	Lys	Phe	Leu		Ara
167	9,5			260					265			-,-		270	<b>-</b>	9
168	Gln	Sor	Ser		Glu	Δen	Cve	Asn		Val	Val	Asn	Thr	_	Glv	T.VC
169	9211	Der	275	GLY	<b>0</b>	ASII	Cys	280	V 44.	<b>V</b> G T	<b>V U T</b>	ASII	285	пеа	O	цуз
170	λτα	λla		λla	Dho	Glu	Glv		Tla	T.011	T.011	Asn		Gln	λen	T.ve
171	Arg	290	PIO	AIG	FILE	GIU	295	Arg	116	пеа	пец	300	FIO	GIII	ASP	цуз
172	Acn		807	Pho	Sor	Val		Tlo	Th x	Gl v	T 011	Arg	Tue	clu.	Aen	λla
173	305	GLY	Ser	FILE	Ser	310	Val	116	1111	GLY	315	Arg	цуз	GIU	ASP	320
174	-	A = ~	m	T 011	Crrc	-	A 7 a	ui a	80-	N.c.v		Gln	T 011	<b>C1</b> n	<b>Cl</b> 111	
	GIY	Arg	ıyı	Leu	325	GLY	Ата	птъ	ser	330	GLY	GIII	Leu	GTII	335	GIY
175	Co.=	Dwa	T1.	<b>al</b> =		m	<b>a</b> 1-	T 011	Dho		A ~ ~	Glu	<b>a</b> 1	C		T1.
176	Ser	PIO	тте		АТА	тър	GIN	Leu		val	ASII	GIU	GIU		THE	тте
177	D===	N	g	340	mb	Wa 1	17.01	T	345	W-1	31 a	<b>a</b> 1	Co	350	17.01	» I o
178	Pro	Arg		PIO	THE	var	vaı	360	GTA	vaı	ALA	Gly		ser	Val	АТА
179	17-1	T	355	D===	m	3	N		a1	G	T	<b>G</b>	365	T	m	m
180	vaı		cys	PIO	Tyr	ASI	_	гаг	GIU	ser	гуѕ	Ser	тте	гуѕ	Tyr	тгр
181	G	370	m	a1	<b>a</b> 1		375	<b>3</b>	a1		<b>a</b>	380	T	T	17.7	3
182	_	Leu	тгр	GIU	GTA		GIN	ASN	GTA	Arg	_	Pro	Leu	Leu	vaı	_
183	385	<b>a</b> 1	a1	m		390		a1	M	<b>a</b> 1	395	<b>3</b>	T	a	T	400
184	ser	GIU	GIY	тгр		гàг	АТА	GIN	Tyr		GLY	Arg	Leu	ser		Leu
185	<b>a</b> 1	<b>a</b> 1	D	a1	405	<b>a</b> 1	ml	Db	m1	410	<b>-1</b> -	T		<b>a</b> 1	415	m\
186	GIU	GIU	Pro	-	ASN	GTÀ	Thr	Pne		val	тте	Leu	ASN		Leu	Thr
187	<b>~</b>			420	<b>a</b> 1	Dh.	m	m	425	T	m1		<b>a</b> 1	430	ml	T
188	ser	Arg	-	АТа	GTA	Pne	Tyr	_	cys	Leu	Thr	Asn	-	Asp	Thr	Leu
189	m	•	435	m1	7	<b>a</b> 1	<b>-</b> 1 -	440	-1-	<b>-1</b> -	<b>a</b> 1	<b>a</b> 1	445	D	<b>3</b>	<b>.</b>
190	Trp	_	Thr	Thr	vaı	GIU		ьys	тте	тте	GIU	Gly	GIU	Pro	ASN	Leu
191		450	<b>D</b>	<b>a</b> 1		**- 7	455				-1	460	m1	<b>-</b>	<b>-</b>	7
192	_	vaı	Pro	GTA	Asn		Thr	АТа	vат	Leu	_	Glu	Thr	Leu	гàг	
193	465			_,	_	470	_	-1	_	_	475		_	_	_	480
194	Pro	Cys	His	Phe		cys	Lys	Pne	Ser		Tyr	Glu	Lys	тyr	_	cys
195	_	_	_		485		_			490	_	_		_	495	~-7
196	Lys	Trp	Asn		Thr	GTĀ	Cys	GIn		Leu	Pro	Ser	GIn	_	GIU	GTÀ
197	_			500		<b>-</b>			505		_		_	510		_
198	Pro	Ser	_	Ala	Phe	Val	Asn	_	Asp	GLu	Asn	Ser	_	Leu	Val	Ser
199	_		515	_	_			520		_			525	_	_	
200	Leu		Leu	Asn	Leu	Val		Arg	Ala	Asp	GLu	Gly	Trp	Tyr	Trp	Cys
201	_	530		_			535		_			540		<u>-</u>	_	
202	_	Val	Lys	Gln	Gly		Phe	Tyr	GŢĀ	Glu		Ala	Ala	Val	Tyr	
203	545				_	550					555	_	<b>_</b>			560
204	Ala	Val	Glu	Glu	_	Lys	Ala	Ala	Gly		Arg	Asp	Val	Ser		Ala
205					565					570					575	

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206	Lys	Ala	Asp	Ala	Ala	Pro	Asp	Glu	Lys	Val	Leu	Asp	Ser	Gly	Phe	Arg	
207				580					585					590			
						_					_	_	9				
208	Glu	Ile	Glu	Asn	Lys	Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	GIX	

## **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/09/095,385*

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Original Text